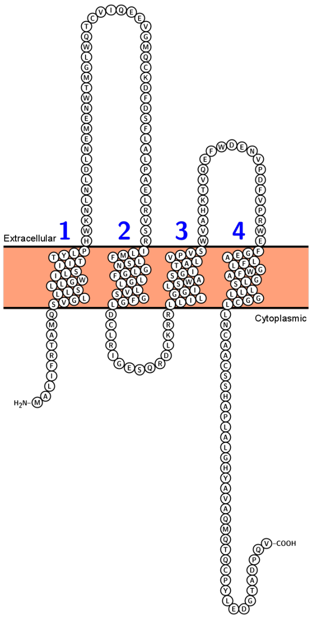
Cube Biotech

Putative claudin-24

Organism: Homo sapiens (Human) | **Gene names:** CLDN24, CLDN21



Entry: A6NM45

Mass: 24.421 Da

Transmembrane: 4

Subcellular location: Cell junction, tight junction {ECO:0000250}. Cell membrane {ECO:0000250}, Multi-pass membrane protein {ECO:0000250}.

Cofactor: -

Extinction coefficient: 2.225

Isoelectric Point: 4.87

PubMed ID: 15815621

Family: -

Function:

Plays a major role in tight junction-specific obliteration of the intercellular space, through calcium-independent cell-adhesion activity. {ECO:0000250}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	No data	**DIBMA 12**	No data
DIBMA Glycerol	No data	**DIBMA Glucosamine**	No data
Amphipol 17	No data	**Amphipol 18**	No data
AASTY 6-45	No data	**AASTY 11-45**	No data
AASTY 6-50	No data	**AASTY 11-50**	No data
AASTY 6- 55	No data	**AASTY 11- 55**	No data
SMALP 502-E	No data	**SMALP 140-I**	No data
SMALP 300	No data	**SMALP 200**	No data
SMALP 140	No data	**DDM**	No data
DM	No data	**LMNG**	No data
Fos-12	No data	**Digitonin-A**	No data
RIPA	No data		

Data from experiment(s): Hek293 membrane pellets 1 %

DIBMA 10	No data	**DIBMA 12**	No data
DIBMA Glycerol	No data	**DIBMA Glucosamine**	No data
Amphipol 17	No data	**Amphipol 18**	No data
AASTY 6-45	No data	**AASTY 11-45**	No data
AASTY 6-50	No data	**AASTY 11-50**	No data
AASTY 6- 55	No data	**AASTY 11- 55**	No data
SMALP 502-E	No data	**SMALP 140-I**	No data
SMALP 300	No data	**SMALP 200**	No data
SMALP 140	No data	**DDM**	No data
DM	No data	**LMNG**	No data
Fos-12	No data	**Digitonin-A**	No data
RIPA	No data		

Involvement in disease:

-

Binding site:

-

Tissue specificity:

-

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MALIFRTAMQSVGLLLSLLGWILSIITTYLPHWKNLNLDLNEMENWTMGLWQTCVIQEEVGMQCKDFDSFLALPAELRVSRILM
FLSNGLGFLGLLVSGFGLDCLRIGESQRDLKRRLLILGGILSWASGITALVPVSWVAHKTVQEFWDENVPDFVPRWEFGEALFLG
WFAGLSLLLGGCLLNCAACSSHAPLALGHYAVAQMQTQCPYLEDGTADPQV

Creditnotes:

The protein visualizations are generated with the help of Protter:
Omasits, U., Ahrens, C.H., MÃ¼ller, S., Wollscheid, B. “Protter: interactive protein feature visualization and integration with experimental proteomic data”. *Bioinformatics*. 2014 Mar 15; **30**(6):884-6. doi: 10.1093/bioinformatics/btt607.

IP and extinction coefficients are gathered from Protparam by ExPASy:
Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D., Bairoch, A. “Protein Identification and Analysis Tools on the ExPASy Server”. (In) *John M. Walker (ed): The Proteomics Protocols Handbook*, Humana Press (2005). pp. 571-607

The basic knowledge is found on UniProt:
The UniProt Consortium. “UniProt: the universal protein knowledgebase in 2021”. *Nucleic Acids Res*. **49**:D1 (2021)
